OIPE

RAW SEQUENCE LISTING DATE: 06/08/2000
PATENT APPLICATION: US/09/580,201 TIME: 13:50:11

Input Set : A:\2314-187.app
Output Set: N:\CRF3\06082000\I580201.raw

See p.p. 1 and 4

Does Not Comply
Corrected Diskette Needed

```
     3 <110> APPLICANT: McIntosh, J. Michael
     4       Olivera, Baldomero M.
     5       Cruz, Lourdes J.
     6       Corpuz, Gloria P.
     7       Jones, Robert M.
     8       Garrett, James E.
    10 <120> TITLE OF INVENTION: Conotoxin Peptides
    12 <130> FILE REFERENCE: Conotoxin Peptides
C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/580,201
C--> 15 <141> CURRENT FILING DATE: 2000-05-26
    17 <150> PRIOR APPLICATION NUMBER: US 60/173,298
    18 <151> PRIOR FILING DATE: 1999-12-28
    20 <150> PRIOR APPLICATION NUMBER: US 60/118,381
    21 <151> PRIOR FILING DATE: 1999-01-29
    23 <150> PRIOR APPLICATION NUMBER: US 09/493,143
    24 <151> PRIOR FILING DATE: 2000-01-28
    26 <160> NUMBER OF SEQ ID NOS: 20
    28 <170> SOFTWARE: PatentIn Ver. 2.0
    30 <210> SEQ ID NO: 1
    31 <211> LENGTH: 14
    32 <212> TYPE: PRT
    33 <213> ORGANISM: Artificial Sequence
    35 <220> FEATURE:
    36 <223> OTHER INFORMATION: Description of Artificial Sequence:generic
    37       conotoxin peptide sequence
    39 <220> FEATURE:
    40 <221> NAME/KEY: PEPTIDE
    41 <222> LOCATION: (1)..(2)
    42 <223> OTHER INFORMATION: Xaa at residue 1 is des-Xaa, Asn, Gln or pyro-Glu;
    43       Xaa at residue 2 is des-Xaa, Gly, Ala, Glu, gamma-
    44       carboxy-Glu, Asp, Asn, Ser, Thr, g-Asn (where g is
    45       glycosylation), g-Ser or g-Thr;
    47 <220> FEATURE:
    48 <221> NAME/KEY: PEPTIDE
    49 <222> LOCATION: (3)..(7)
    50 <223> OTHER INFORMATION: Xaa at residue 3 is Val, Ala, Gly, Leu, Ile, Ser,
    51       Thr, g-Asn, g-Ser or g-Thr; Xaa at residue is Phe,
    52       Tyr, meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr,
    53       di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
    55 <220> FEATURE:
    56 <221> NAME/KEY: PEPTIDE
    57 <222> LOCATION: (7)
    58 <223> OTHER INFORMATION: nitro-Tyr, Trp (D or L), neo-Trp, halo-Trp (D or
    59       L), any synthetic aromatic amino acid, an
    60       aliphatic amino acid bearing linear or branched
    61       saturated hydrocarbon chains such as Leu (D or L),
W--> 62       Ile and
```

residue location number needs to be present here.

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```
     64 <220> FEATURE:
     65 <221> NAME/KEY: PEPTIDE
     66 <222> LOCATION: (7)..(8)
     67 <223> OTHER INFORMATION: Val or non-natural derivatives of the aliphatic
     68       amino acid; Xaa at residue 8 is Lys, Arg,
     69       homolysine, homoarginine, ornithine, nor-Lys, His,
     70       N-methyl-Lys, N,N'-dimethyl-Lys,
W--> 71       N,N',N''-trimethyl-Lys,
     73 <220> FEATURE:
     74 <221> NAME/KEY: PEPTIDE
     75 <222> LOCATION: (8)..(9)
     76 <223> OTHER INFORMATION: any synthetic basic amino acid, Ser, Thr, g-Ser,
     77       g-Thr or any hydroxylated synthetic residue; Xaa
     78       at residue 9 is an aliphatic amino acids bearing
     79       linear or branched saturated hydrocarbon chains
W--> 80       such
     82 <220> FEATURE:
     83 <221> NAME/KEY: PEPTIDE
     84 <222> LOCATION: (9)
     85 <223> OTHER INFORMATION: as Leu (D or L), Ile and Val or non-natural
     86       derivatives of the aliphatic amino acid, Met, Phe,
     87       Tyr, meta-Tyr, ortho-Tyr, nor-Tyr, mono-halo-Tyr,
     88       di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
W--> 89       nitro-Tyr,
     91 <220> FEATURE:
     92 <221> NAME/KEY: PEPTIDE
     93 <222> LOCATION: (9)..(11)
     94 <223> OTHER INFORMATION: Trp (D or L), neo-Trp, halo-Trp (D or L) or any
     95       synthetic aromatic amino acid; Xaa at residue 11
     96       is His, Ser, Thr, g-Ser, g-Thr, an aliphatic amino
     97       acid bearing linear or branched saturated
     99 <220> FEATURE:
    100 <221> NAME/KEY: NP_BIND
    101 <222> LOCATION: (11)
    102 <223> OTHER INFORMATION: hydrocarbon chains such as Leu (D or L), Ile and
    103       Val, non-natural derivatives of the aliphatic
    104       amino acid, Phe, Tyr, meta-Tyr, ortho-Tyr,
    105       nor-Tyr, mono-halo-Tyr, di-halo-Tyr, O-sulpho-Tyr,
    107 <220> FEATURE:
    108 <221> NAME/KEY: PEPTIDE
    109 <222> LOCATION: (11)..(14)
    110 <223> OTHER INFORMATION: O-phospho-Tyr, nitro-Tyr, Trp (D or L), neo-Trp,
    111       halo-Trp (D or L) or a synthetic aromatic amino
    112       acid; Xaa at residue 12 is Pro, hydroxy- Pro (Hyp)
    113       or g-Hyp; Xaa at residue 14 is des-Xaa, Gly, Ala,
    115 <220> FEATURE:
    116 <221> NAME/KEY: PEPTIDE
    117 <222> LOCATION: (14)
    118 <223> OTHER INFORMATION: Lys, Arg, homolysine, homoarginine, ornithine,
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```
      nor-Lys, His, N-methyl-Lys, N,N'-dimethyl-Lys,
      N,N',N''-trimethyl-Lys or any synthetic basic
      amino acid.
<400> SEQUENCE: 1
Xaa Xaa Xaa Cys Cys Gly Xaa Xaa Xaa Cys Xaa Xaa Cys Xaa
  1               5                  10
<210> SEQ ID NO: 2
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Conus marmoreus
<220> FEATURE:
<221> NAME/KEY: PEPTIDE
<222> LOCATION: (7)..(8)
<223> OTHER INFORMATION: Xaa at residue 7 is Tyr, mono-halo-Tyr,
      di-halo-Tyr, O-sulpho-Tyr, O-Phospho-Tyr or
      nitro-Tyr; Xaa at residue 8 is Lys, N-methyl-Lys,
      N,N-dimethyl-Lys or N,N,N-trimethyl Lys
<220> FEATURE:
<221> NAME/KEY: PEPTIDE
<222> LOCATION: (12)
<223> OTHER INFORMATION: Xaa at residue 12 is Pro or hydroxy-Pro.
<400> SEQUENCE: 2
Asn Gly Val Cys Cys Gly Xaa Xaa Leu Cys His Xaa Cys
  1               5                  10
<210> SEQ ID NO: 3
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Conus marmoreus
<220> FEATURE:
<221> NAME/KEY: PEPTIDE
<222> LOCATION: (6)..(7)
<223> OTHER INFORMATION: Xaa at residue 6 is Tyr, mono-halo-Tyr,
      di-halo-Tyr, O-sulpho-Tyr, O-Phospho-Tyr or
      nitro-Tyr; Xaa at residue 7 is Lys, N-methyl-Lys,
      N,N-dimethyl-Lys or N,N,N-trimethyl Lys
<220> FEATURE:
<221> NAME/KEY: PEPTIDE
<222> LOCATION: (11)
<223> OTHER INFORMATION: Xaa at residue 11 is Pro or hydroxy-Pro
<400> SEQUENCE: 3
Gly Val Cys Cys Gly Xaa Xaa Leu Cys His Xaa Cys
  1               5                  10
<210> SEQ ID NO: 4
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Unknown
<220> FEATURE:
<223> OTHER INFORMATION: Description of Unknown Organism:unknown Conus
      species
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183 <220> FEATURE:
184 <221> NAME/KEY: PEPTIDE
185 <222> LOCATION: (6)..(7)
186 <223> OTHER INFORMATION: Xaa at residue 6 is Tyr, mono-halo-Tyr,
187       di-halo-Tyr, O-sulpho-Tyr, O-Phospho-Tyr or
188       nitro-Tyr; Xaa at residue 8 is Lys, N-methyl-Lys,
189       N,N-dimethyl-Lys or N,N,N-trimethyl Lys.
191 <220> FEATURE:
192 <221> NAME/KEY: PEPTIDE
193 <222> LOCATION: (11)
194 <223> OTHER INFORMATION: Xaa at residue 11 is Pro or hydroxy-Pro
196 <400> SEQUENCE: 4
W--> 197 Gly Val Cys Cys Gly Xaa Xaa Leu Cys His Xaa Cys
198   1               5                  10
201 <210> SEQ ID NO: 5
202 <211> LENGTH: 11
203 <212> TYPE: PRT
204 <213> ORGANISM: Conus bandanus
206 <220> FEATURE:
207 <221> NAME/KEY: PEPTIDE
208 <222> LOCATION: (6)..(7)
209 <223> OTHER INFORMATION: Xaa at residue 6 is Tyr, mono-halo-Tyr,
210       di-halo-Tyr, O-sulpho-Tyr, O-phospho-Tyr,
211       nitro-Tyr; Xaa at residue 7 is Lys, N-methy-Lys,
212       N,N-dimethyl-Lys or N,N,N-trimethyl-Lys;
214 <220> FEATURE:
215 <221> NAME/KEY: PEPTIDE
216 <222> LOCATION: (10)
217 <223> OTHER INFORMATION: Xaa at residue 10 is Pro or hydroxy-Pro (Hyp)
219 <400> SEQUENCE: 5
W--> 220 Ala Cys Cys Gly Xaa Xaa Lys Cys Ser Xaa Cys
221   1               5                  10
224 <210> SEQ ID NO: 6
225 <211> LENGTH: 13
226 <212> TYPE: PRT
227 <213> ORGANISM: Conus textile
229 <220> FEATURE:
230 <221> NAME/KEY: PEPTIDE
231 <222> LOCATION: (1)..(11)
232 <223> OTHER INFORMATION: Xaa at residue 1 is Gln or pyro-Glu; Xaa at
233       residue 6 is Tyr, mono-halo-Tyr, di-halo-Tyr,
234       O-sulpho-Tyr, O-phospho-Tyr, nitro-Tyr; Xaa at
235       residue 11 is Pro or hydroxy-Pro (Hyp)
237 <400> SEQUENCE: 6
W--> 238 Xaa Thr Cys Cys Gly Xaa Arg Met Cys Val Xaa Cys Gly
239   1               5                  10
242 <210> SEQ ID NO: 7
243 <211> LENGTH: 13
244 <212> TYPE: PRT
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residues are located at location 5 and 6, not 6 and 7 as listed.

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PATENT APPLICATION: US/09/580,201 TIME: 13:50:11

Input Set : A:\2314-187.app
Output Set: N:\CRF3\06082000\I580201.raw

245 <213> ORGANISM: Conus pennaceus
247 <220> FEATURE:
248 <221> NAME/KEY: PEPTIDE
249 <222> LOCATION: (7)..(11)
250 <223> OTHER INFORMATION: Xaa at residue 7 is Lys, N-methy-Lys,
251 N,N-dimethyl-Lys or N,N,N-trimethyl-Lys; Xaa at
252 residue 11 is Pro or hydroxy-Pro (Hyp)
254 <400> SEQUENCE: 7
W--> 255 Ser Thr Cys Cys Gly Phe Xaa Met Cys Ile Xaa Cys Arg
256 1 5 10
259 <210> SEQ ID NO: 8
260 <211> LENGTH: 25
261 <212> TYPE: DNA
262 <213> ORGANISM: Conus marmoreus
264 <220> FEATURE:
265 <221> NAME/KEY: modified_base
266 <222> LOCATION: (14)
267 <223> OTHER INFORMATION: i
269 <400> SEQUENCE: 8
W--> 270 caggatccaa yggngtbtgy tgygg 25
273 <210> SEQ ID NO: 9
274 <211> LENGTH: 28
275 <212> TYPE: DNA
276 <213> ORGANISM: Conus marmoreus
278 <220> FEATURE:
279 <221> NAME/KEY: modified_base
280 <222> LOCATION: (26)
281 <223> OTHER INFORMATION: i
283 <400> SEQUENCE: 9
W--> 284 ctggatccgg rtgrcavary ttrtancc 28
287 <210> SEQ ID NO: 10
288 <211> LENGTH: 23
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Description of Artificial Sequence:universal
294 primer
296 <400> SEQUENCE: 10
297 aagctcgagt aacaacgcag agt 23
300 <210> SEQ ID NO: 11
301 <211> LENGTH: 805
302 <212> TYPE: DNA
303 <213> ORGANISM: Conus marmoreus
305 <220> FEATURE:
306 <221> NAME/KEY: CDS
307 <222> LOCATION: (82)..(264)
309 <400> SEQUENCE: 11
310 ggcgaataca cctggcaggt actcaacgaa cttcaggaca cattcttttc acctggacac 60
312 tggaaactga caacaggcag a atg cgc tgt ctc cca gtc ttg atc att ctt 111

VERIFICATION SUMMARY DATE: 06/08/2000
PATENT APPLICATION: US/09/580,201 TIME: 13:50:12

Input Set : A:\2314-187.app
Output Set: N:\CRF3\06082000\I580201.raw

OK

L:74 M:270 C: Current Application Number differs, Replaced Application Number
L:75 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:62 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:71 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:80 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:89 M:259 W: Field exceeds allowed number of lines, <223> Other Information:
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:170 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:238 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:270 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:284 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9